

**Primary structure of human nonmuscle-type cofilin  
(AC: P23528)**

MASGVAVSDG VIKVFNDMKV RKSSTPEEVK KRKKAVLFCL SEDKKNIILE  
EGKEILVGDV  
GQTVD**DPYAT** FVKMLPDKDC RYALYDATYE TKESKKEDLV FIFWAPESAP  
LKS**KM**YASS  
KDAIKKKLTG IKHELQANCY EEVKDRCTLA EKLGGSAVIS LEGKPL

The underlined portions are the sites analyzed for  
sequence by MS and MS/MS.

Met Ala Ser Gly Val Ala Val Ser Asp Gly Val Ile Lys Val Phe Asn

5 10 15

Asp Met Lys Val Arg Lys Ser Ser Thr Pro Glu Glu Val Lys Lys Arg

20 25 30

Lys Lys Ala Val Leu Phe Cys Leu Ser Glu Asp Lys Lys Asn Ile Ile

35 40 45

Leu Glu Glu Gly Lys Glu Ile Leu Val Gly Asp Val Gly Gln Thr Val

50 55 60

Asp Asp Pro Tyr Ala Thr Phe Val Lys Met Leu Pro Asp Lys Asp Cys

65 70 75 80

Arg Tyr Ala Leu Tyr Asp Ala Thr Tyr Glu Thr Lys Glu Ser Lys Lys

85 90 95

Glu Asp Leu Val Phe Ile Phe Trp Ala Pro Glu Ser Ala Pro Leu Lys

100 105 110

Ser Lys Met Ile Tyr Ala Ser Ser Lys Asp Ala Ile Lys Lys Lys Leu

115 120 125

Thr Gly Ile Lys His Glu Leu Gln Ala Asn Cys Tyr Glu Glu Val Lys

130 135 140

Asp Arg Cys Thr Leu Ala Glu Lys Leu Gly Gly Ser Ala Val Ile Ser

145 150 155 160

Leu Glu Gly Lys Pro Leu

165

**Fig. 1**

**cDNA of human placental nonmuscle-type cofilin  
(AC: D00682)**

atggcctccg gtgtggctgt ctctgatggt gtcataagg tttcaacga catgaagg 60  
cgtaagtctt caacgccaga ggaggtgaag aagcgcaaga aggccgtgct cttctgcctg 120  
agtgaggaca agaagaacat catcctggag gagggcaagg agatcctggt gggcgatgtg 180  
ggccagactg tcgacgatcc ctacgccacc tttgtcaaga tgctgccaga taaggactgc 240  
cgctatgccc tctatgatgc aacctatgag accaaggaga gcaagaagga ggtatctgg 300  
tttatcttct gggcccccga gtctgcgeccc cttaaagagca aaatgattta tgccagctcc 360  
aaggacgcca tcaagaagaa gctgacaggg atcaagcatg aattgcaagc aaactgctac 420  
gaggaggtca aggaccgctg caccctggca gagaagctgg gggcagtgc ggtcatctcc 480  
ctggaggcga agcctttgtg a 501

The underlined portions are the sites where two oligomers were synthesized as primers.

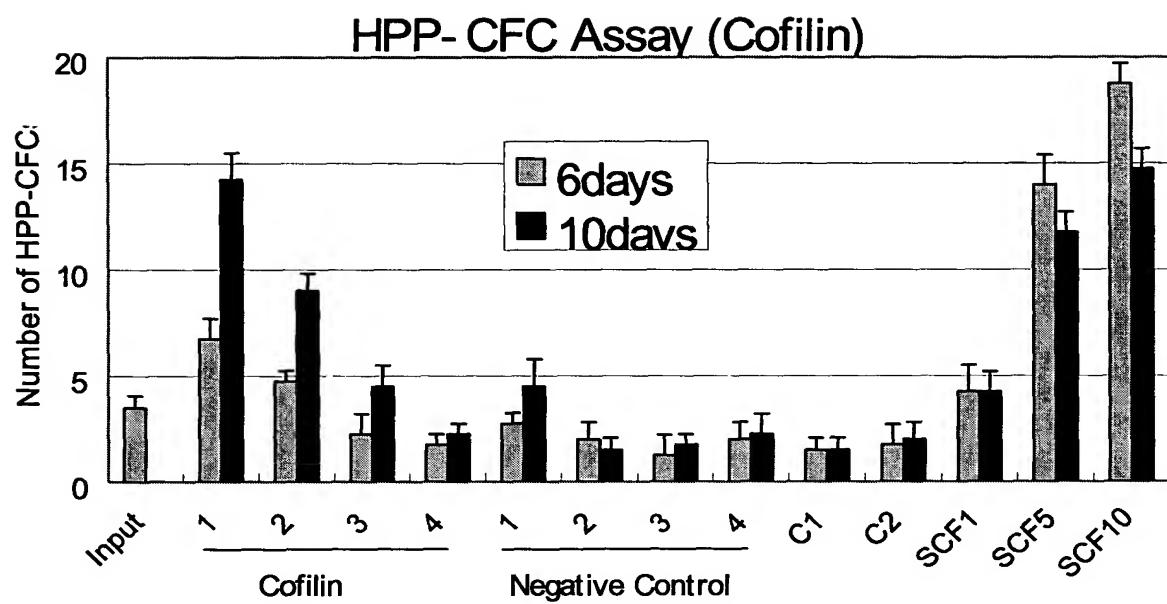
**Fig. 2**

**Alignment of the base sequences for nonmuscle-type cofilin derived from human placenta (upper) and from human S6 cells (lower).**

Placental cDNA	10	20	30	40	50
TGTTCAACGA	1 ATGGCCTCCG	GTGTGGCTGT	CTCTGATGGT	GTCATCAAGG	
S6 cDNA	50				
TGTTCAACGA	1 ATGGCCTCCG	GTGTGGCTGT	CTCTGATGGT	GTCATCAAGG	
Placental cDNA	60	70	80	90	100
AAGCGCAAGA	51 CATGAAGGTG	CGTAAGTCTT	CAACGCCAGA	GGAGGTGAAG	
S6 cDNA	100				
	51 CATGAAGGTG	CGTAAGTCTT	CAACGCCAGA	GGAGGTGAAG	
Placental cDNA	110	120	130	140	150
CATCCTGGAG	101 AGGCCGTGCT	CTTCTGCCTG	AGTGAGGACA	AGAAGAACAT	
S6 cDNA	150				
	101 AGGCCGTGCT	CTTCTGCCTG	AGTGAGGACA	AGAAGAACAT	
Placental cDNA	160	170	180	190	200
TCGACGATCC	151 GAGGGCAAGG	AGATCCTGGT	GGCGATGTG	GGCCAGACTG	
S6 cDNA	200				
	151 GAGGGCAAGG	AGATCCTGGT	GGCGATGTG	GGCCAGACTG	
Placental cDNA	210	220	230	240	250
CGCTATGCC	201 CTACGCCACC	TTTGTCAAGA	TGCTGCCAGA	TAAGGACTGC	
S6 cDNA	250				
	201 CTACGCCACC	TTTGTCAAGA	TGCTGCCAGA	TAAGGACTGC	
Placental cDNA	260	270	280	290	300
GGATCTGGTG	251 TCTATGATGC	AACCTATGAG	ACCAAGGAGA	GCAAGAACAGA	
S6 cDNA	300				
	251 TCTATGATGC	AACCTATGAG	ACCAAGGAGA	GCAAGAACAGA	
Placental cDNA	310	320	330	340	350
AAATGATTAA	301 TTTATCTTCT	GGGCCCGA	GTCTGCGCCC	CTTAAGAGCA	
S6 cDNA	350				
	301 TTTATCTTCT	GGGCCCGA	GTCTGCGCCC	CTTAAGAGCA	
Placental cDNA	360	370	380	390	400
ATCAAGCATG	351 TGCCAGCTCC	AAGGACGCCA	TCAAGAACAGA	GCTGACAGGG	
S6 cDNA	400				
	351 TGCCAGCTCC	AAGGACGCCA	TCAAGAACAGA	GCTGACAGGG	
Placental cDNA	410	420	430	440	450
CACCCCTGGCA	401 AATTGCAAGC	AAACTGCTAC	GAGGAGGTCA	AGGACCGCTG	
S6 cDNA	450				
	401 AATTGCAAGC	AAACTGCTAC	GAGGAGGTCA	AGGACCGCTG	
Placental cDNA	460	470	480	490	500
AGCCTTGTG	451 GAGAAGCTGG	GGGGCAGTGC	GGTCATCTCC	CTGGAGGGCA	
S6 cDNA	500				
	451 GAGAAGCTGG	GGGGCAGTGC	GGTCATCTCC	CTGGAGGGCA	
Placental cDNA	510	520	530	540	550
S6 cDNA	501 A.....	.....	.....	550	
	501 A.....	.....	.....	550	

The two bases that differ between the two sequences are marked by shadowing and are both due to silent mutation.

**Fig. 3**



**Fig. 4**

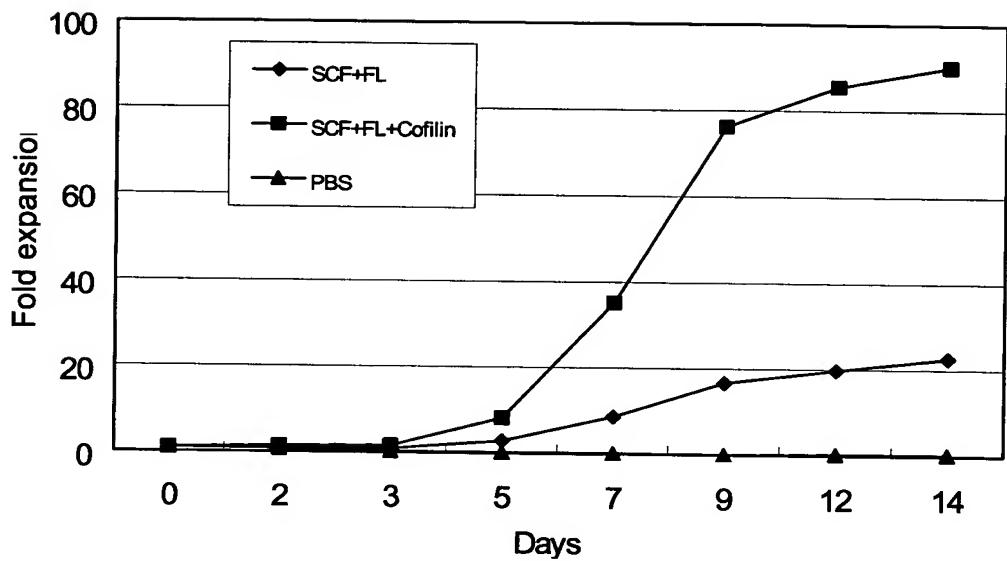
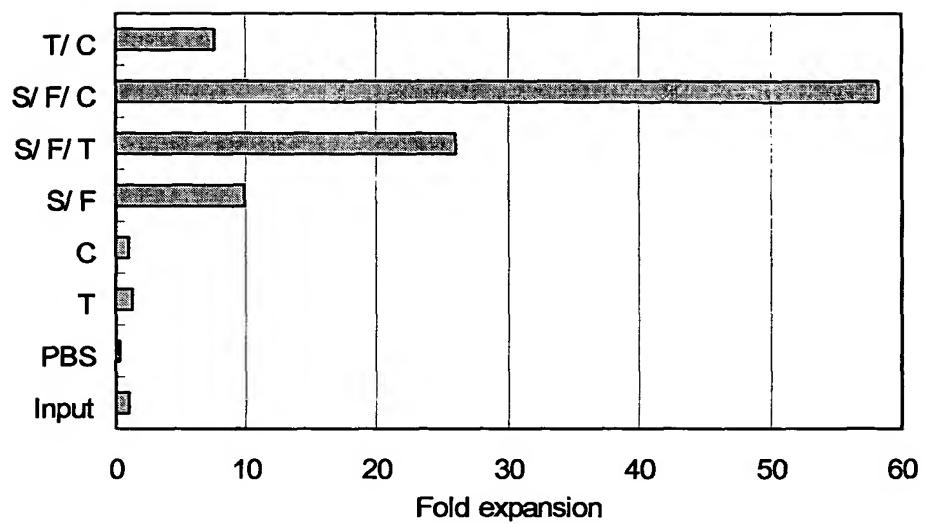
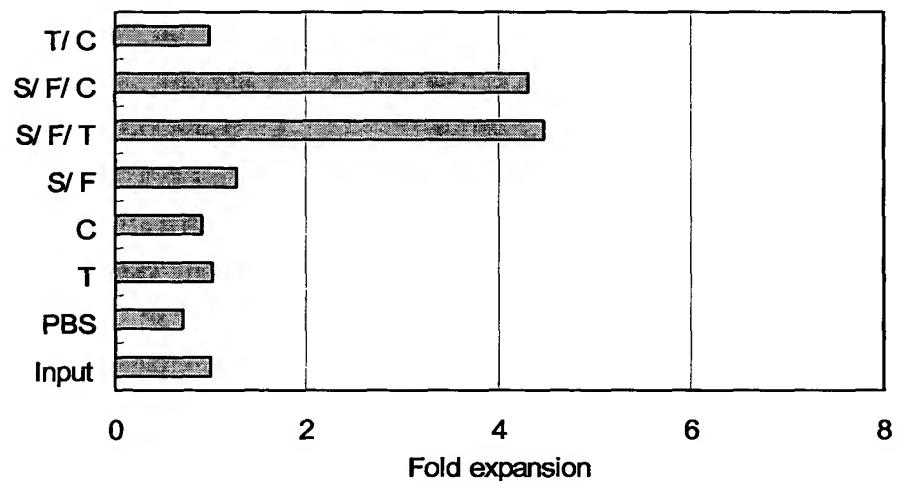


Fig. 5

**A**

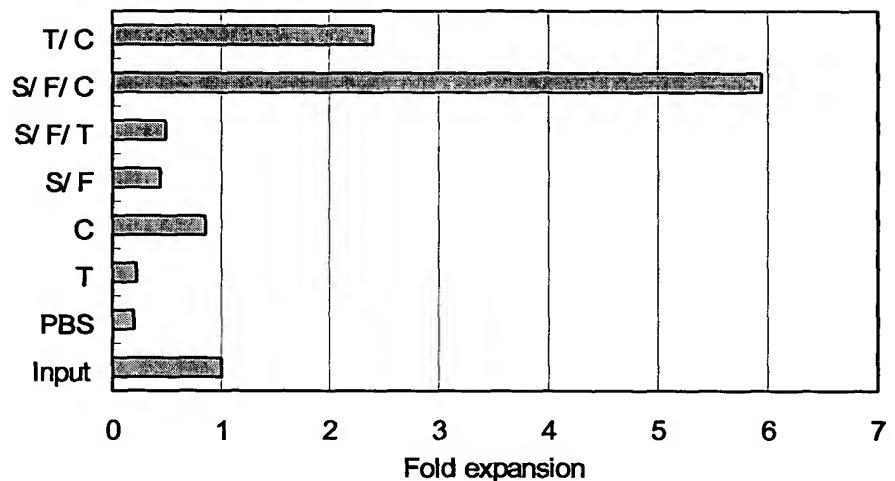


**B**



**Fig. 6**

C



D

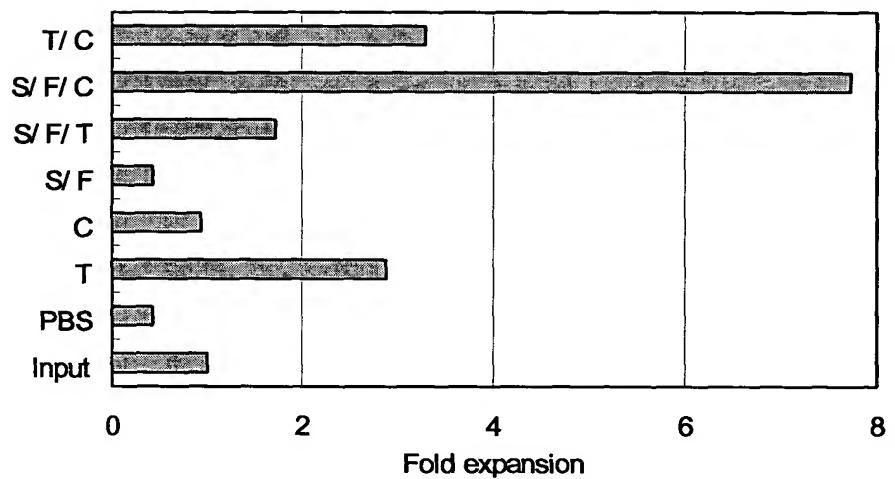


Fig. 6 (Cont.)

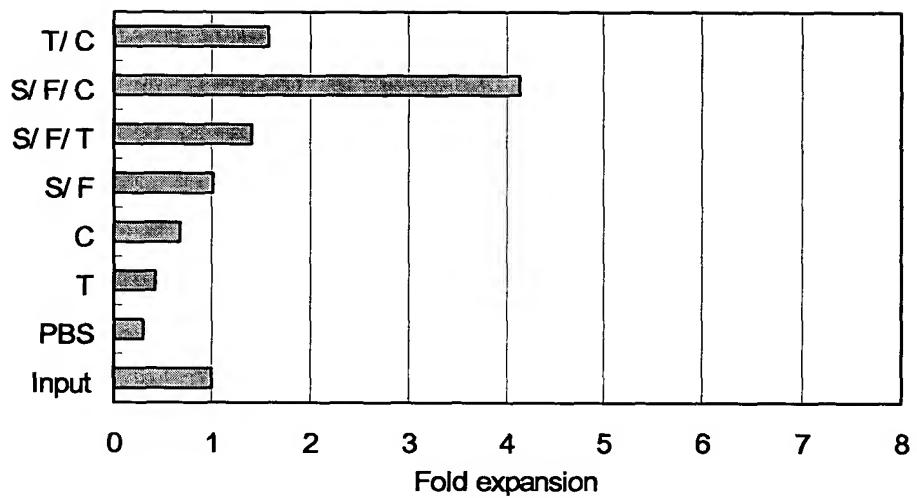
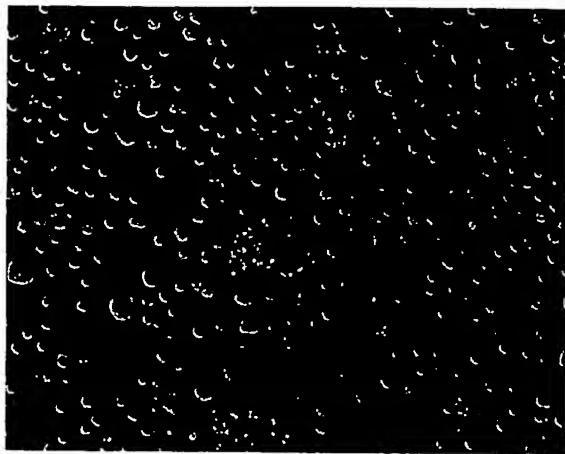
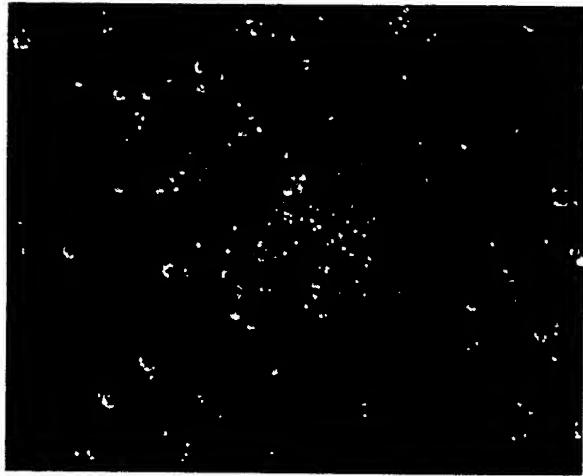


Fig. 7



**Fig. 8**



**Fig. 9**